



Rec'd PCT/PTO 14 SEP 2005

SEQUENCE LISTING

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Blumwald, Eduardo

<120> IMPROVED TRANSPORTERS AND THEIR USES

<130> 023070-127310US

<140> US 10/520,497

<141> 2003-07-09

<150> WO PCT/US2003/021549

<151> 2003-07-09

<150> US 60/395,662

<151> 2002-07-12

<160> 22

<170> PatentIn version 3.3

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<211> 1614

<212> DNA

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<212> PRT
<213> Arabidopsis thaliana

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His Ala Ser Val Val Ala Leu Asn Leu Phe Val Ala Leu Leu Cys Ala
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Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
35 40 45

Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
50 55 60

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
65 70 75 80

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
85 90 95

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
100 105 110

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
115 120 125

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
 130 135 140

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
 145 150 155 160

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
 165 170 175

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe
 180 185 190

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala
 195 200 205

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu
 210 215 220

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu
 225 230 235 240

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu
 245 250 255

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly
 260 265 270

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp
 275 280 285

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala
 290 295 300

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met
 305 310 315 320

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly
 325 330 335

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly
 340 345 350

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys
 355 360 365

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp
 370 375 380

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn
 385 390 395 400

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
 405 410 415

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
 420 425 430

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
 435 440 445

Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile
 450 455 460

Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn
 465 470 475 480

Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg
 485 490 495

Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro
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20 25 30

Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
35 40 45

Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
50 55 60

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
65 70 75 80

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
85 90 95

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
100 105 110

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
115 120 125

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
130 135 140

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
145 150 155 160

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
165 170 175

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe
180 185 190

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala
195 200 205

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu
210 215 220

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu
225 230 235 240

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu
245 250 255

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly

260

265

270

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp
 275 280 285

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala
 290 295 300

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met
 305 310 315 320

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly
 325 330 335

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly
 340 345 350

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys
 355 360 365

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp
 370 375 380

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn
 385 390 395 400

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
 405 410 415

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
 420 425 430

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
 435 440 445

Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile
 450 455 460

Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn
 465 470 475 480

Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg
 485 490 495

Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Cys Phe Met Arg Pro
 500 505 510

Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr
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 20 25 30

Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
 35 40 45

Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
 50 55 60

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
 65 70 75 80

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
 85 90 95

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
 100 105 110

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
 115 120 125

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
 130 135 140

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
 145 150 155 160

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
 165 170 175

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe
 180 185 190

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala
 195 200 205

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu
 210 215 220

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu
 225 230 235 240

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu
 245 250 255

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly
 260 265 270

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp
 275 280 285

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala
 290 295 300

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met
 305 310 315 320

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly
 325 330 335

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly
 340 345 350

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys
 355 360 365

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp
 370 375 380

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn
 385 390 395 400

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
 405 410 415

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
 420 425 430

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
 435 440 445

Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile
 450 455 460

Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn
 465 470 475 480

Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg
 485 490 495

Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro
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Val Phe Gly Gly Arg Gly Phe Val Pro
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<400> 8

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          20           25           30

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Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
          35           40           45

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Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
50           55           60

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Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
65           70           75           80

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Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
 85 90 95

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
 100 105 110

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
 115 120 125

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
 130 135 140

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
 145 150 155 160

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
 165 170 175

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe
 180 185 190

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala
 195 200 205

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu
 210 215 220

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu
 225 230 235 240

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu
 245 250 255

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly
 260 265 270

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp
 275 280 285

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala
 290 295 300

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met
 305 310 315 320

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly
 325 330 335

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly
 340 345 350

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys
 355 360 365

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp
 370 375 380

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn
 385 390 395 400

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
 405 410 415

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
 420 425 430

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
 435 440 445

Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile
 450 455 460

Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn
 465 470 475 480

Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu
 485 490

<210> 9
 <211> 1362
 <212> DNA
 <213> Artificial

<220>
 <223> Modified AtNHX1 DL-3.

<400> 9
 atgttgatt ctctagtgtc gaaactgcct tcgttatcga catctgatca cgcttctgtg 60
 gttgcgttga atctctttgt tgcacttctt tgtgcttgta ttgttcttg tcatcttttg 120
 gaagagaata gatggatgaa cgaatccatc accgccttgt tgattgggct aggcactggt 180
 gttaccattt tgttgattag taaaggaaaa agctcgcac ttctcgtctt tagtgaagat 240

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cttttcttca tataatctttt gccacccatt atattcaatg cagggtttca agtaaaaaag 300
aagcagtttt tccgcaatth cgtgactatt atgctttttg gtgctgttgg gactattatt 360
tcttgacaaa tcatatctct aggtgtaaca cagttcttta agaagttgga cattggaacc 420
tttgacttgg gtgattatct tgctattggg gccatatttg ctgcaacaga ttcagtatgt 480
acactgcagg ttctgaatca agacgagaca cctttgcttt acagtcttgt attcggagag 540
gggtgttgta atgatgcaac gtcagttgtg gtcttcaacg cgattcagag ctttgatctc 600
actcacctaa accacgaagc tgcttttcat cttcttgtaa acttcttgta tttgtttctc 660
ctaagtacct tgcttgggtg tgcaaccggg ctgataagtg cgtatgttat caagaagcta 720
tactttggaa ggcaactcaac tgaccgagag gttgccctta tgatgcttat ggcgtatctt 780
tcttatatgc ttgctgagct tttcgacttg agcggtatcc tcaactgtgtt tttctgtggg 840
attgtgatgt cccattacac atggcacaat gtaacggaga gctcaagaat aacaacaaag 900
catacctttg caactttgtc atttcttgcg gagacattta ttttcttgta tgttggaatg 960
gatgccttgg acattgacaa gtggagatcc gtgagtgaca caccgggaac atcgatcgca 1020
gtgagctcaa tcctaattggg tctggtcatg gttggaagag cagcgttcgt ctttccgtta 1080
tcgtttctat ctaacttagc caagaagaat caaagcgaga aaatcaactt taacatgcag 1140
gttgatgattt ggtgggtctgg tctcatgaga ggtgctgtat ctatggctct tgcatacaac 1200
aagtttacaa gggccgggca cacagatgta cgcgggaatg caatcatgat cagagtacg 1260
ataactgtct gtcttttttag cacagtgggtg tttggtatgc tgaccaaacc actcataagc 1320
tacctattac cgcaccagaa cgccaccacg agcatgttat ct 1362

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<210> 10
<211> 454
<212> PRT
<213> Artificial

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<220>
<223> Putative amino acid encoded by modified AtNHX1 DL-3.
<400> 10

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Met Leu Asp Ser Leu Val Ser Lys Leu Pro Ser Leu Ser Thr Ser Asp
1           5           10           15

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His Ala Ser Val Val Ala Leu Asn Leu Phe Val Ala Leu Leu Cys Ala
          20           25           30

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Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
          35           40           45

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Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
50 55 60

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
65 70 75 80

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
85 90 95

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
100 105 110

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
115 120 125

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
130 135 140

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
145 150 155 160

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
165 170 175

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe
180 185 190

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala
195 200 205

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu
210 215 220

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu
225 230 235 240

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu
245 250 255

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly
260 265 270

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp
275 280 285

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala

290

295

300

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met
305 310 315 320

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly
325 330 335

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly
340 345 350

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys
355 360 365

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp
370 375 380

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn
385 390 395 400

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
405 410 415

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
420 425 430

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
435 440 445

Thr Thr Ser Met Leu Ser
450

<210> 11
<211> 1566
<212> DNA
<213> Artificial

<220>
<223> Modified AtNHX1 NDL-1 cDNA.

<400> 11
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ggatcatcttt tggaagagaa tagatggatg aacgaatcca tcaccgcctt gttgattggg 120
ctaggcactg gtgttaccat tttgttgatt agtaaaggaa aaagctcgca tcttctcgtc 180
tttagtgaag atcttttctt catatatctt ttgccacca ttatattcaa tgcagggttt 240
caagtaaaaa agaagcagtt tttccgcaat ttcgtgacta ttatgctttt tgggtgctgtt 300

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gggactatta tttcttgac aatcatatct ctaggtgtaa cacagttctt taagaagttg 360
gacattggaa cctttgactt gggtgattat cttgctattg gtgccatatt tgctgcaaca 420
gattcagtat gtacactgca ggttctgaat caagacgaga cacctttgct ttacagtctt 480
gtattcggag aggggtgttg gaatgatgca acgtcagttg tggctctcaa cgcgattcag 540
agctttgatc tcaactcacct aaaccacgaa gctgcttttc atcttcttgg aaacttcttg 600
tatttgtttc tcctaagtac cttgcttggg gctgcaaccg gtctgataag tgcgtatggt 660
atcaagaagc tatacttttg aaggcactca actgaccgag aggttgccct tatgatgctt 720
atggcgtatc tttcttatat gcttgotgag cttttcgact tgagcgggat cctcaactgtg 780
tttttctgtg gtattgtgat gtcccattac acatggcaca atgtaacgga gagctcaaga 840
ataacaacaa agcatacctt tgcaactttg tcatttcttg cggagacatt tattttcttg 900
tatgttggaa tggatgcctt ggacattgac aagtggagat ccgtgagtga cacaccggga 960
acatcgatcg cagtgagctc aatcctaata ggtctgggtc tggttggaag agcagcgttc 1020
gtctttccgt tatcgtttct atctaactta gccagaaga atcaaagcga gaaaatcaac 1080
ttaacatgc aggttgtgat ttggtggtct ggtctcatga gaggtgctgt atctatggct 1140
cttgcataca acaagtttac aaggggccggg cacacagatg tacgcgggaa tgcaatcatg 1200
atcacgagta cgataactgt ctgtcttttt agcacagtgg tgtttggtat gctgaccaa 1260
ccactcataa gctacctatt accgcaccag aacgccacca cgagcatgtt atctgatgac 1320
aacaccccaa aatccataca tatccctttg ttggaccaag actcgttcat tgagccttca 1380
gggaaccaca atgtgcctcg gcctgacagt atacgtggct tcttgacacg gccactcga 1440
accgtgcatt actactggag acaatttgat gactccttca tgcgaccgt ctttggaggt 1500
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<210> 12
<211> 522
<212> PRT
<213> Artificial

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<220>
<223> Putative amino acid encoded by modified AtNHX1 NDL-1 cDNA.

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<400> 12

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Met Ala Ser Val Val Ala Leu Asn Leu Phe Val Ala Leu Leu Cys Ala
1           5           10          15

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Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu

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20

25

30

Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
35 40 45

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
50 55 60

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
65 70 75 80

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
85 90 95

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
100 105 110

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
115 120 125

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
130 135 140

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
145 150 155 160

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Phe
165 170 175

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala
180 185 190

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu
195 200 205

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu
210 215 220

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu
225 230 235 240

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly
245 250 255

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp
260 265 270

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala
 275 280 285

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met
 290 295 300

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly
 305 310 315 320

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly
 325 330 335

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys
 340 345 350

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp
 355 360 365

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn
 370 375 380

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
 385 390 395 400

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
 405 410 415

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
 420 425 430

Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile
 435 440 445

Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn
 450 455 460

Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg
 465 470 475 480

Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro
 485 490 495

Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr
 500 505 510

Glu Arg Asn Pro Pro Asp Leu Ser Lys Ala
 515 520

<210> 13
 <211> 1410
 <212> DNA
 <213> Artificial

<220>
 <223> NDL-2 cDNA.

<400> 13
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 actattatgc tttttggtgc tgttgggact attatttctt gcacaatcat atctctaggt 180
 gtaacacagt tctttaagaa gttggacatt ggaacctttg acttgggtga ttatcttgct 240
 attggtgcca tatttgctgc aacagattca gtatgtacac tgcaggttct gaatcaagac 300
 gagacacctt tgctttacag tcttgtattc ggagagggtg ttgtgaatga tgcaacgtca 360
 gttgtggtct tcaacgcgat tcagagcttt gatctcactc acctaaacca cgaagctgct 420
 tttcatcttc ttggaaactt cttgtatttg tttctcctaa gtaccttgct tgggtgctgca 480
 accggtctga taagtgcgta tgttatcaag aagctatact ttggaaggca ctcaactgac 540
 cgagagggtg cccttatgat gcttatggcg tatctttctt atatgcttgc tgagcttttc 600
 gacttgagcg gtatcctcac tgtgtttttc tgtggtattg tgatgtccca ttacacatgg 660
 cacaatgtaa cggagagctc aagaataaca acaaagcata cctttgcaac tttgtcattt 720
 cttgcggaga catttatattt cttgtatggt ggaatggatg ccttggacat tgacaagtgg 780
 agatccgtga gtgacacacc gggaacatcg atcgcagtga gctcaatcct aatgggtctg 840
 gtcatggttg gaagagcagc gttcgtcttt ccgttatcgt ttctatctaa cttagccaag 900
 aagaatcaaa gcgagaaaat caactttaac atgcagggtg tgatttggtg gtctggtctc 960
 atgagagggtg ctgtatctat ggctcttgca tacaacaagt ttacaagggc cgggcacaca 1020
 gatgtacgcg ggaatgcaat catgatcacg agtacgataa ctgtctgtct ttttagcaca 1080
 gtggtggttg gtatgctgac caaaccactc ataagctacc tattaccgca ccagaacgcc 1140
 accacgagca tgttatctga tgacaacacc ccaaaatcca tacatatccc tttgttggac 1200
 caagactcgt tcattgagcc ttcagggaac cacaatgtgc ctcggcctga cagtatacgt 1260
 ggcttcttga cacggcccac tcgaaccgtg cattactact ggagacaatt tgatgactcc 1320
 ttcattgcgac ccgtcttttg aggtcgtggc tttgtaccct ttgttccagg ttctccaact 1380
 gagagaaacc ctctgatct tagtaaggct 1410

<210> 14
 <211> 470
 <212> PRT
 <213> Artificial

<220>
 <223> Putative amino acid encoded by modified AtNHX1 NDL-2 cDNA.

<400> 14

Met Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp Leu Phe Phe Ile
 1 5 10 15

Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe Gln Val Lys Lys
 20 25 30

Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu Phe Gly Ala Val
 35 40 45

Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly Val Thr Gln Phe
 50 55 60

Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly Asp Tyr Leu Ala
 65 70 75 80

Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys Thr Leu Gln Val
 85 90 95

Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu Val Phe Gly Glu
 100 105 110

Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe Asn Ala Ile Gln
 115 120 125

Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala Phe His Leu Leu
 130 135 140

Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu Leu Gly Ala Ala
 145 150 155 160

Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu Tyr Phe Gly Arg
 165 170 175

His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu Met Ala Tyr Leu
 180 185 190

Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly Ile Leu Thr Val

195

200

205

Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp His Asn Val Thr
 210 215 220

Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala Thr Leu Ser Phe
 225 230 235 240

Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met Asp Ala Leu Asp
 245 250 255

Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly Thr Ser Ile Ala
 260 265 270

Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly Arg Ala Ala Phe
 275 280 285

Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys Lys Asn Gln Ser
 290 295 300

Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp Trp Ser Gly Leu
 305 310 315 320

Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn Lys Phe Thr Arg
 325 330 335

Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met Ile Thr Ser Thr
 340 345 350

Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly Met Leu Thr Lys
 355 360 365

Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala Thr Thr Ser Met
 370 375 380

Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile Pro Leu Leu Asp
 385 390 395 400

Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn Val Pro Arg Pro
 405 410 415

Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg Thr Val His Tyr
 420 425 430

Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro Val Phe Gly Gly
 435 440 445

Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr Glu Arg Asn Pro
 450 455 460

Pro Asp Leu Ser Lys Ala
 465 470

<210> 15
 <211> 1323
 <212> DNA
 <213> Artificial

<220>
 <223> NDL-3 cDNA.

<400> 15
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 actattatatt cttgcacaat catatctcta ggtgtaacac agttctttta gaagttggac 120
 attggaacct ttgacttggg tgattatctt gctattgggtg ccatatttgc tgcaacagat 180
 tcagtatgta cactgcaggt tctgaatcaa gacgagacac ctttgcttta cagtcttgta 240
 ttcggagagg gtgttgtaga tgatgcaacg tcagttgttg tcttcaacgc gattcagagc 300
 tttgatctca ctcacctaaa ccacgaagct gcttttcac tctttggaaa cttcttgat 360
 ttgtttctcc taagtacctt gcttgggtgct gcaaccgggc tgataagtgc gtatgttatc 420
 aagaagctat actttggaag gcaactcaact gaccgagagg ttgcccttat gatgcttatg 480
 gcgtatcttt cttatatgct tgctgagctt ttcgacttga gcggtatcct cactgtgttt 540
 ttctgtggta ttgtgatgtc ccattacaca tggcacaatg taacggagag ctcaagaata 600
 acaacaaagc atacctttgc aactttgtca tttcttgagg agacatttat tttcttgat 660
 gttggaatgg atgccttggc cattgacaag tggagatccg tgagtgcac accgggaaca 720
 tcgatcgcag tgagctcaat cctaattgggt ctggtcatgg ttggaagagc agcgttcgtc 780
 tttccgttat cgtttctatc taacttagcc aagaagaatc aaagcgagaa aatcaacttt 840
 aacatgcagg ttgtgatttg gtggtctggt ctcatgagag gtgctgtatc tatggctctt 900
 gcatacaaca agttttacaag ggccggggcac acagatgtac gcgggaatgc aatcatgatc 960
 acgagtacga taactgtctg tcttttttagc acagtgggtg ttggtatgct gaccaaacca 1020
 ctcataagct acctattacc gcaccagaac gccaccacga gcatgttatc tgatgacaac 1080
 accccaaaat ccatacatat ccctttgttg gaccaagact cgttcattga gccttcaggg 1140
 aaccacaatg tgcctcggcc tgacagtata cgtggcttct tgacacggcc cactcgaacc 1200
 gtgcattact actggagaca atttgatgac tccttcatgc gaccctctt tggaggctgt 1260

ggctttgtac cctttgttcc aggttctcca actgagagaa accctcctga tcttagtaag 1320
gct 1323

<210> 16
<211> 439
<212> PRT
<213> Artificial

<220>
<223> Putative amino acid encoded by modified AtNHX1 NDL-3 cDNA.

<400> 16

Met Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu Phe
1 5 10 15

Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly Val
20 25 30

Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly Asp
35 40 45

Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys Thr
50 55 60

Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu Val
65 70 75 80

Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Trp Val Phe Asn Ala
85 90 95

Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala Phe His
100 105 110

Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu Leu Gly
115 120 125

Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu Tyr Phe
130 135 140

Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu Met Ala
145 150 155 160

Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly Ile Leu
165 170 175

Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp His Asn
180 185 190

Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala Thr Leu
 195 200 205

Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met Asp Ala
 210 215 220

Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly Thr Ser
 225 230 235 240

Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly Arg Ala
 245 250 255

Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys Lys Asn
 260 265 270

Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Trp Ile Trp Trp Ser Gly
 275 280 285

Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn Lys Phe Thr
 290 295 300

Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met Ile Thr Ser
 305 310 315 320

Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly Met Leu Thr
 325 330 335

Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala Thr Thr Ser
 340 345 350

Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile Pro Leu Leu
 355 360 365

Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn Val Pro Arg
 370 375 380

Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg Thr Val His
 385 390 395 400

Tyr Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro Val Phe Gly
 405 410 415

Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr Glu Arg Asn
 420 425 430

Pro Pro Asp Leu Ser Lys Ala
435

<210> 17
<211> 35
<212> DNA
<213> Artificial

<220>
<223> Putative amino acid encoded by modified AtNHX1 NDL-3 cDNA.

<400> 17
ggagacaatt tgatgactgc ttcattgcgac ccgtc 35

<210> 18
<211> 35
<212> DNA
<213> Artificial

<220>
<223> Primer SM-23-R

<400> 18
gacgggtcgc atgaagcagt catcaaattg tctcc 35

<210> 19
<211> 38
<212> DNA
<213> Artificial

<220>
<223> Primer EXCH-5

<400> 19
agctaggatc cggatctaga agaagataac aatgttgg 38

<210> 20
<211> 33
<212> DNA
<213> Artificial

<220>
<223> Primer EXCH-DL-1

<400> 20
agctgaattc ctaggttaca aagccacgac ctc 33

<210> 21
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Primer EXCH-DL-2

<400> 21
agctgaattc ctacaagaag ccacgtatac tg

32

<210> 22
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Primer EXCH-DL-3

<400> 22
agctgaattc ctaagataac atgctcgtgg tg

32